



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/817,431
Source: TFW
Date Processed by STIC: 4/8/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/817,431
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics _____ Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 _____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 _____ Misaligned Amino _____ Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 _____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 _____ PatentIn 2.0 _____ "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 _____ Invalid <213> _____ Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 _____ Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 _____ PatentIn 2.0 _____ "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 _____ Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFWO

RAW SEQUENCE LISTING

DATE: 04/08/2004

PATENT APPLICATION: US/10/817,431

TIME: 16:14:49.

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

4 <110> APPLICANT: Degussa AG
 7 <120> TITLE OF INVENTION: Process for the production of L-amino acids using strains of
 the
 8 Enterobacteriaceae family
 11 <130> FILE REFERENCE: 020489 BT
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/817,431
 C--> 14 <141> CURRENT FILING DATE: 2004-04-05
 14 <160> NUMBER OF SEQ ID NOS: 8
 17 <170> SOFTWARE: PatentIn version 3.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 30
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Synthetic sequence
 26 <220> FEATURE:
 W--> 27 <221> NAME/KEY: Primer
 28 <222> LOCATION: (1)..(30)
 29 <223> OTHER INFORMATION: yfiD1
 32 <220> FEATURE:
 W--> 33 <221> NAME/KEY: Restriction site
 34 <222> LOCATION: (9)..(14)
 35 <223> OTHER INFORMATION: XbaI site
 38 <400> SEQUENCE: 1
 39 gaacaaatct agaaattaag ccgggggaggc
 41 <210> SEQ ID NO: 2
 42 <211> LENGTH: 24
 43 <212> TYPE: DNA
 44 <213> ORGANISM: Synthetic sequence
 47 <220> FEATURE:
 W--> 48 <221> NAME/KEY: Primer
 49 <222> LOCATION: (1)..(24)
 50 <223> OTHER INFORMATION: yfiD2
 53 <220> FEATURE:
 W--> 54 <221> NAME/KEY: Restriction site
 55 <222> LOCATION: (8)..(13)
 56 <223> OTHER INFORMATION: HindIII site
 59 <400> SEQUENCE: 2
 60 gctacttaag ctttacaggc tttc
 62 <210> SEQ ID NO: 3
 64 <211> LENGTH: 431
 65 <212> TYPE: DNA
 66 <213> ORGANISM: Escherichia coli
 69 <220> FEATURE:
 W--> 70 <221> NAME/KEY: yfiD PCR product
 71 <222> LOCATION: (1)..(431)

Does Not Comply
 Corrected Diskette Needed

Invalid
 Response

mandatory <213> Response
 Artificial
 has to be either
 Unknown or Genus/Species,
 Please see item #
 10 on error summary
 sheet.

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

72 <223> OTHER INFORMATION:

75 <220> FEATURE:

76 <221> NAME/KEY: CDS

77 <222> LOCATION: (36)..(419)

78 <223> OTHER INFORMATION: open reading frame yfiD

W--> 81 <400> 3

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82 gaacaaatct agaaattaag ccggggaggc atcac atg att aca ggt atc cag      53
83                               Met Ile Thr Gly Ile Gln
84                               1           5
86 att act aaa gcc gct aac gac gat ctg ctg aac tct ttc tgg ctg ctg      101
87 Ile Thr Lys Ala Ala Asn Asp Asp Leu Leu Asn Ser Phe Trp Leu Leu
88           10           15           20
90 gac agc gaa aaa ggc gaa gcg cgt tgc atc gtt gca aaa gca ggt tat      149
91 Asp Ser Glu Lys Gly Glu Ala Arg Cys Ile Val Ala Lys Ala Gly Tyr
92           25           30           35
94 gca gaa gat gaa gtg gtt gca gta agc aaa ctg ggt gac att gaa tac      197
95 Ala Glu Asp Glu Val Val Ala Val Ser Lys Leu Gly Asp Ile Glu Tyr
96           40           45           50
98 cgt gaa gtt cca gta gaa gtg aaa cca gaa gtt cgc gtt gaa ggt ggt      245
99 Arg Glu Val Pro Val Glu Val Lys Pro Glu Val Arg Val Glu Gly Gly
100 55           60           65           70
102 caa cac ctg aac gtt aac gtt ctg cgt cgc gaa act ctg gaa gat gca      293
103 Gln His Leu Asn Val Asn Val Leu Arg Arg Glu Thr Leu Glu Asp Ala
104           75           80           85
106 gtt aag cat ccg gaa aaa tat ccg cag ctg acc atc cgt gta tcc ggt      341
107 Val Lys His Pro Glu Lys Tyr Pro Gln Leu Thr Ile Arg Val Ser Gly
108           90           95           100
110 tat gca gtt cgc ttt aac tct ctg act ccg gaa cag cag cgc gac gtt      389
111 Tyr Ala Val Arg Phe Asn Ser Leu Thr Pro Glu Gln Gln Arg Asp Val
112           105           110           115
114 atc gct cgt acc ttt act gaa agc ctg taa agcttaagta gc      431
115 Ile Ala Arg Thr Phe Thr Glu Ser Leu
116           120           125
119 <210> SEQ ID NO: 4
120 <211> LENGTH: 127
121 <212> TYPE: PRT
122 <213> ORGANISM: Escherichia coli
125 <400> SEQUENCE: 4
126 Met Ile Thr Gly Ile Gln Ile Thr Lys Ala Ala Asn Asp Asp Leu Leu
127 1           5           10           15
129 Asn Ser Phe Trp Leu Leu Asp Ser Glu Lys Gly Glu Ala Arg Cys Ile
130           20           25           30
132 Val Ala Lys Ala Gly Tyr Ala Glu Asp Glu Val Val Ala Val Ser Lys
133           35           40           45
135 Leu Gly Asp Ile Glu Tyr Arg Glu Val Pro Val Glu Val Lys Pro Glu
136           50           55           60
138 Val Arg Val Glu Gly Gly Gln His Leu Asn Val Asn Val Leu Arg Arg
139 65           70           75           80
141 Glu Thr Leu Glu Asp Ala Val Lys His Pro Glu Lys Tyr Pro Gln Leu

```

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

```

142                85                90                95
144 Thr Ile Arg Val Ser Gly Tyr Ala Val Arg Phe Asn Ser Leu Thr Pro
145                100                105                110
147 Glu Gln Gln Arg Asp Val Ile Ala Arg Thr Phe Thr Glu Ser Leu
148                115                120                125
150 <210> SEQ ID NO: 5
151 <211> LENGTH: 28
152 <212> TYPE: DNA
153 <213> ORGANISM: Synthetic sequence
156 <220> FEATURE:
W--> 157 <221> NAME/KEY: Primer
158 <222> LOCATION: (1)..(28)
159 <223> OTHER INFORMATION: pflB1
162 <220> FEATURE:
W--> 163 <221> NAME/KEY: Restriction site
164 <222> LOCATION: (5)..(10)
165 <223> OTHER INFORMATION: XbaI site
168 <400> SEQUENCE: 5
169 ccactctaga aggtaggtgt tacatgtc
171 <210> SEQ ID NO: 6
172 <211> LENGTH: 27
173 <212> TYPE: DNA
174 <213> ORGANISM: Synthetic sequence
177 <220> FEATURE:
W--> 178 <221> NAME/KEY: Primer
179 <222> LOCATION: (1)..(27)
180 <223> OTHER INFORMATION: pflB2
183 <220> FEATURE:
W--> 184 <221> NAME/KEY: Restriction site
185 <222> LOCATION: (13)..(18)
186 <223> OTHER INFORMATION: HindIII site
189 <400> SEQUENCE: 6
190 cgatttcagt caaagcttat tacatag
193 <210> SEQ ID NO: 7
194 <211> LENGTH: 2325
195 <212> TYPE: DNA
196 <213> ORGANISM: Escherichia coli
199 <220> FEATURE:
W--> 200 <221> NAME/KEY: pflB PCR product
201 <222> LOCATION: (1)..(2325)
202 <223> OTHER INFORMATION:
205 <220> FEATURE:
206 <221> NAME/KEY: CDS
207 <222> LOCATION: (24)..(2306)
208 <223> OTHER INFORMATION: pflB coding region
W--> 211 <400> 7
212 ccactctaga aggtaggtgt tac atg tcc gag ctt aat gaa aag tta gcc aca
213                Met Ser Glu Leu Asn Glu Lys Leu Ala Thr
214                1                5                10

```

28

27

53

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

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Input Set : A:\SEQUENCE LISTING.txt

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216	gcc	tgg	gaa	ggt	ttt	acc	aaa	ggt	gac	tgg	cag	aat	gaa	'gta	aac	gtc	101
217	Ala	Trp	Glu	Gly	Phe	Thr	Lys	Gly	Asp	Trp	Gln	Asn	Glu	Val	Asn	Val	
218					15					20					25		
220	cgt	gac	ttc	att	cag	aaa	aac	tac	act	ccg	tac	gag	ggt	gac	gag	tcc	149
221	Arg	Asp	Phe	Ile	Gln	Lys	Asn	Tyr	Thr	Pro	Tyr	Glu	Gly	Asp	Glu	Ser	
222				30					35					40			
224	ttc	ctg	gct	ggc	gct	act	gaa	gcg	acc	acc	acc	ctg	tgg	gac	aaa	gta	197
225	Phe	Leu	Ala	Gly	Ala	Thr	Glu	Ala	Thr	Thr	Thr	Leu	Trp	Asp	Lys	Val	
226			45						50					55			
228	atg	gaa	ggc	gtt	aaa	ctg	gaa	aac	cgc	act	cac	gcg	cca	gtt	gac	ttt	245
229	Met	Glu	Gly	Val	Lys	Leu	Glu	Asn	Arg	Thr	His	Ala	Pro	Val	Asp	Phe	
230		60					65					70					
232	gac	acc	gct	gtt	gct	tcc	acc	atc	acc	tct	cac	gac	gct	ggc	tac	atc	293
233	Asp	Thr	Ala	Val	Ala	Ser	Thr	Ile	Thr	Ser	His	Asp	Ala	Gly	Tyr	Ile	
234	75					80					85				90		
236	aac	aag	cag	ctt	gag	aaa	atc	gtt	ggt	ctg	cag	act	gaa	gct	ccg	ctg	341
237	Asn	Lys	Gln	Leu	Glu	Lys	Ile	Val	Gly	Leu	Gln	Thr	Glu	Ala	Pro	Leu	
238				95						100					105		
240	aaa	cgt	gct	ctt	atc	ccg	ttc	ggt	ggt	atc	aaa	atg	atc	gaa	ggt	tcc	389
241	Lys	Arg	Ala	Leu	Ile	Pro	Phe	Gly	Gly	Ile	Lys	Met	Ile	Glu	Gly	Ser	
242				110					115					120			
244	tgc	aaa	gcg	tac	aac	cgc	gaa	ctg	gat	ccg	atg	atc	aaa	aaa	atc	ttc	437
245	Cys	Lys	Ala	Tyr	Asn	Arg	Glu	Leu	Asp	Pro	Met	Ile	Lys	Lys	Ile	Phe	
246			125						130					135			
248	act	gaa	tac	cgt	aaa	act	cac	aac	cag	ggc	gtg	ttc	gac	gtt	tac	act	485
249	Thr	Glu	Tyr	Arg	Lys	Thr	His	Asn	Gln	Gly	Val	Phe	Asp	Val	Tyr	Thr	
250		140					145					150					
252	ccg	gac	atc	ctg	cgt	tgc	cgt	aaa	tct	ggt	gtt	ctg	acc	ggt	ctg	cca	533
253	Pro	Asp	Ile	Leu	Arg	Cys	Arg	Lys	Ser	Gly	Val	Leu	Thr	Gly	Leu	Pro	
254	155					160					165				170		
256	gat	gca	tat	ggc	cgt	ggc	cgt	atc	atc	ggt	gac	tac	cgt	cgc	gtt	gcg	581
257	Asp	Ala	Tyr	Gly	Arg	Gly	Arg	Ile	Ile	Gly	Asp	Tyr	Arg	Arg	Val	Ala	
258				175						180					185		
260	ctg	tac	ggt	atc	gac	tac	ctg	atg	aaa	gac	aaa	ctg	gca	cag	ttc	act	629
261	Leu	Tyr	Gly	Ile	Asp	Tyr	Leu	Met	Lys	Asp	Lys	Leu	Ala	Gln	Phe	Thr	
262				190						195				200			
264	tct	ctg	cag	gct	gat	ctg	gaa	aac	ggc	gta	aac	ctg	gaa	cag	act	atc	677
265	Ser	Leu	Gln	Ala	Asp	Leu	Glu	Asn	Gly	Val	Asn	Leu	Glu	Gln	Thr	Ile	
266			205						210					215			
268	cgt	ctg	cgc	gaa	gaa	atc	gct	gaa	cag	cac	cgc	gct	ctg	ggt	cag	atg	725
269	Arg	Leu	Arg	Glu	Glu	Ile	Ala	Glu	Gln	His	Arg	Ala	Leu	Gly	Gln	Met	
270		220					225					230					
272	aaa	gaa	atg	gct	gcg	aaa	tac	ggc	tac	gac	atc	tct	ggt	ccg	gct	acc	773
273	Lys	Glu	Met	Ala	Ala	Lys	Tyr	Gly	Tyr	Asp	Ile	Ser	Gly	Pro	Ala	Thr	
274	235					240					245				250		
276	aac	gct	cag	gaa	gct	atc	cag	tgg	act	tac	ttc	ggc	tac	ctg	gct	gct	821
277	Asn	Ala	Gln	Glu	Ala	Ile	Gln	Trp	Thr	Tyr	Phe	Gly	Tyr	Leu	Ala	Ala	
278				255						260				265			
280	gtt	aag	tct	cag	aac	ggt	gct	gca	atg	tcc	ttc	ggt	cgt	acc	tcc	acc	869

RAW SEQUENCE LISTING

DATE: 04/08/2004

PATENT APPLICATION: US/10/817,431

TIME: 16:14:49

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

```

281 Val Lys Ser Gln Asn Gly Ala Ala Met Ser Phe Gly Arg Thr Ser Thr
282                270                275                280
284 ttc ctg gat gtg tac atc gaa cgt gac ctg aaa gct ggc aag atc acc      917
285 Phe Leu Asp Val Tyr Ile Glu Arg Asp Leu Lys Ala Gly Lys Ile Thr
286                285                290                295
288 gaa caa gaa gcg cag gaa atg gtt gac cac ctg gtc atg aaa ctg cgt      965
289 Glu Gln Glu Ala Gln Glu Met Val Asp His Leu Val Met Lys Leu Arg
290                300                305                310
292 atg gtt cgc ttc ctg cgt act ccg gaa tac gat gaa ctg ttc tct ggc      1013
293 Met Val Arg Phe Leu Arg Thr Pro Glu Tyr Asp Glu Leu Phe Ser Gly
294 315                320                325                330
296 gac ccg atc tgg gca acc gaa tct atc ggt ggt atg ggc ctc gac ggt      1061
297 Asp Pro Ile Trp Ala Thr Glu Ser Ile Gly Gly Met Gly Leu Asp Gly
298                335                340                345
300 cgt acc ctg gtt acc aaa aac agc ttc cgt ttc ctg aac acc ctg tac      1109
301 Arg Thr Leu Val Thr Lys Asn Ser Phe Arg Phe Leu Asn Thr Leu Tyr
302                350                355                360
304 acc atg ggt ccg tct ccg gaa ccg aac atg acc att ctg tgg tct gaa      1157
305 Thr Met Gly Pro Ser Pro Glu Pro Asn Met Thr Ile Leu Trp Ser Glu
306                365                370                375
308 aaa ctg ccg ctg aac ttc aag aaa ttc gcc gct aaa gtg tcc atc gac      1205
309 Lys Leu Pro Leu Asn Phe Lys Lys Phe Ala Ala Lys Val Ser Ile Asp
310                380                385                390
312 acc tct tct ctg cag tat gag aac gat gac ctg atg cgt ccg gac ttc      1253
313 Thr Ser Ser Leu Gln Tyr Glu Asn Asp Asp Leu Met Arg Pro Asp Phe
314 395                400                405                410
316 aac aac gat gac tac gct att gct tgc tgc gta agc ccg atg atc gtt      1301
317 Asn Asn Asp Asp Tyr Ala Ile Ala Cys Cys Val Ser Pro Met Ile Val
318                415                420                425
320 ggt aaa caa atg cag ttc ttc ggt gcg cgt gca aac ctg gcg aaa acc      1349
321 Gly Lys Gln Met Gln Phe Phe Gly Ala Arg Ala Asn Leu Ala Lys Thr
322                430                435                440
324 atg ctg tac gca atc aac ggc ggc gtt gac gaa aaa ctg aaa atg cag      1397
325 Met Leu Tyr Ala Ile Asn Gly Gly Val Asp Glu Lys Leu Lys Met Gln
326                445                450                455
328 gtt ggt ccg aag tct gaa ccg atc aaa ggc gat gtc ctg aac tat gat      1445
329 Val Gly Pro Lys Ser Glu Pro Ile Lys Gly Asp Val Leu Asn Tyr Asp
330                460                465                470
332 gaa gtg atg gag cgc atg gat cac ttc atg gac tgg ctg gct aaa cag      1493
333 Glu Val Met Glu Arg Met Asp His Phe Met Asp Trp Leu Ala Lys Gln
334 475                480                485                490
336 tac atc act gca ctg aac atc atc cac tac atg cac gac aag tac agc      1541
337 Tyr Ile Thr Ala Leu Asn Ile Ile His Tyr Met His Asp Lys Tyr Ser
338                495                500                505
340 tac gaa gcc tct ctg atg gcg ctg cac gac cgt gac gtt atc cgc acc      1589
341 Tyr Glu Ala Ser Leu Met Ala Leu His Asp Arg Asp Val Ile Arg Thr
342                510                515                520
344 atg gcg tgt ggt atc gct ggt ctg tcc gtt gct gct gac tcc ctg tct      1637
345 Met Ala Cys Gly Ile Ala Gly Leu Ser Val Ala Ala Asp Ser Leu Ser

```

VERIFICATION SUMMARY

DATE: 04/08/2004

PATENT APPLICATION: US/10/817,431

TIME: 16:14:50

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\04082004\J817431.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:33 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:48 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:54 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:70 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:81 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:72
L:157 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:163 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:178 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:184 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:200 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:211 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:202